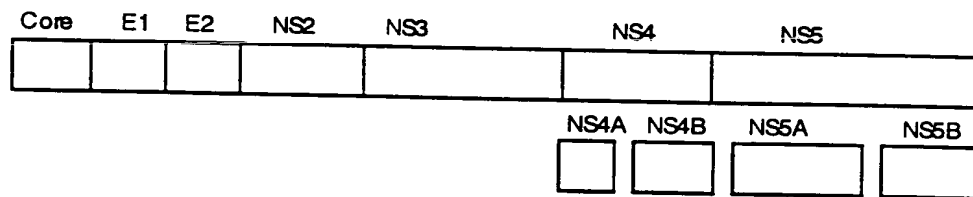


FIGURE 1



666260" 2E4/0460

FIGURE 2

SEQ. ID. NO:1

MSHVAVENALGLDQQFAGLDLNSSDNQSGGSTASKGRYIPPHLRNREATRGFYDKDSSGWSSSKDKDAYSSFGSRSDSRGKSSFFS  
DRGSGSRGRFDDRGRSDYDGIGSRGDRSGFGKFERGGNSRWCDKSEDDWSKPLPPSERLEQELFSGGNTGINFEKYDDIPVEATG  
NNCPPHIESFSDVEMGEIIMGNIELTRYTRPTPVQKHAIPPIKEKRDLMACAQTGSGKTA AFLLPILSQIYSDGPGEALRAMKENG  
RYGRRKQYPISLVLAPTRELAVQIYEEARKFSYRSRVRPCVVYGGADIGQQIRDLERGCHLLVATPGRLVDMMERGKIGLDFCKYL  
VLDEADRMLDMGFEPQIRRIVEQDTMPPKGV RHTMMFSATFPKEIQMLARDFLDEYIFLAVGRVGSTSENITQKVVWVEESDKRSF  
LLDLLNATGKDSLTLVFVETKKGADSLEDFLYHEGYACTSIHGDRSQORDREEALHQFRSGKSPILVATAVAARGLDISNVKHVIN  
FDLPSDIEEYVHRIGRTGRVGNLGLATSFNERNINITKDLLDLLVEAKQEVPSWLENMAYEHYKSSRGRSKSSRFSGGFGARDY  
ROSSGASSSSFSSSRASSRSRGGGGHGSSRGFGGGGYGGFYNSDGYGGNYNSQGVDDWGN

SEQ. ID. NO:2

GSTSENITQKVVWVEESDKRSFLDLLNATGKDSLTLVFVETKKGADSLEDFLYHEGYACTSIHGDRSQORDREEALHQFRSGKSPI  
LVATAVAARGLDISNVKHVINFDLPSDIEEYVHRIGRTGRVGNLGLATSFNERNINITKDLLDLLVEAKQEVPSWLENMAYEHY  
KSSRGRSKSSRFSGGFGARDYROSSGASSSSFSSSRASSRSRGGGGHGSSRGFGGGGYGGFYNSDGYGGNYNSQGVDDWGN

55250-2440450

FIGURE 3

SEQ. ID. NO:3

VGSTSENITQKVWVEESDKRSFLLDLLNATGKDSLTLVFVETKKGADSLEDFLYHEGYACTSIHGDRSQRDREEALHQFRSGKSP  
ILVATAVAARGLDISNVKHVINFDLPSDIEEYVHRIGRTGRVGNLGLAT

66250" 25420160

FIGURE 4

## SEQ. ID. NO:4

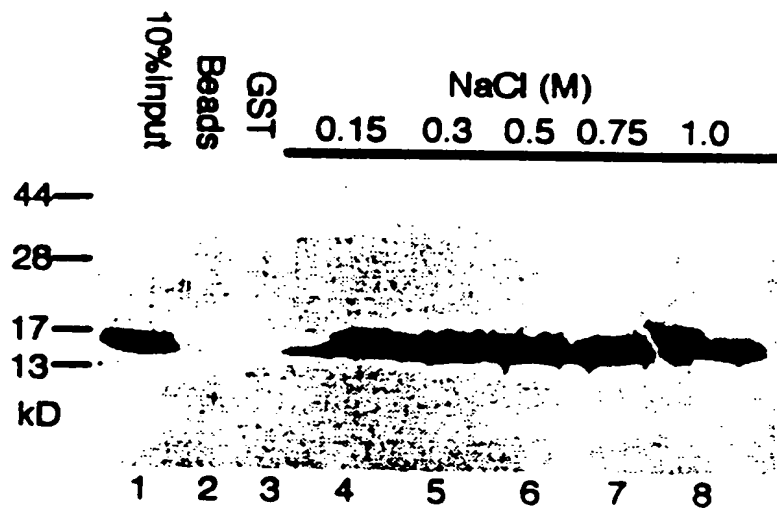
1 atggatgata gagaggatct ggtgtaccag gcgaagctgg ccgagcaggc tgagcgatac  
 61 gacgaaatgg tggagtcaat gaagaaagta gcagggatgg atgtggagct gacagttgaa  
 121 gaaagaaacc tcctatctgt tgcataataag aatgtgattg gagctagaag agcctcctgg  
 181 agaataatca gcagcattga acagaaagaa gaaaacaagg gaggagaaga caagctaaaa  
 241 atgattcggg aatatcggca aatgggttgag actgagctaa agttaatctg ttgtgacatt  
 301 ctggatgtac tggacaaaca cctcattcca gcagctaaca ctggcgagtc caagggtttc  
 361 tattataaaa tgaaagggga ctaccacagg tatctggcag aatttgccac aggaaacgac  
 421 aggaaggagg ctgcggagaa cagcctagtg gcttataaag ctgctagtga tattgcaatg  
 481 acagaacttc caccaacgca tcctattcgc ttaggtcttg ctctcaattt ttccgtattc  
 541 tactacgaaa ttcttaattc ccctgaccgt gcctgcaggt tggcaaaagc agcttttgat  
 601 gatgcaattg cagaactgga tacgtgagt gaagaaagct ataaggactc tacacttacc  
 661 atgcagttgt tacgtgataa tctgacacta tggacttcag acatgcaggg tgacggtgaa  
 721 gagcagaata aagaagcgct gcaggacgtg gaagacgaaa atcagtgaga cataagccaa  
 781 caagagaaac ca

## SEQ. ID. NO:5

translation="MDDREDLVYQAKLAEQAERYDEMVESMKKVAGMDVELTVEERNL  
 LSVAYKNVIGARRASWRIISSIEQKEENKGGEDKLKMIREYRQMVETELKLICCDILD  
 VLDKHLIPAANTGESKVFYYKMGDYHRYLAEFATGNDRKEAAENSLVAYKAASDIAM  
 TELPPTHPIRLGLALNFSVFYYEILNSPDRACRLAKAAFDDAIAELDTLSEESYKDST  
 LIMQLLRDNLTLWTSMDMQGDGEEQNKEALQDVEDENQ"

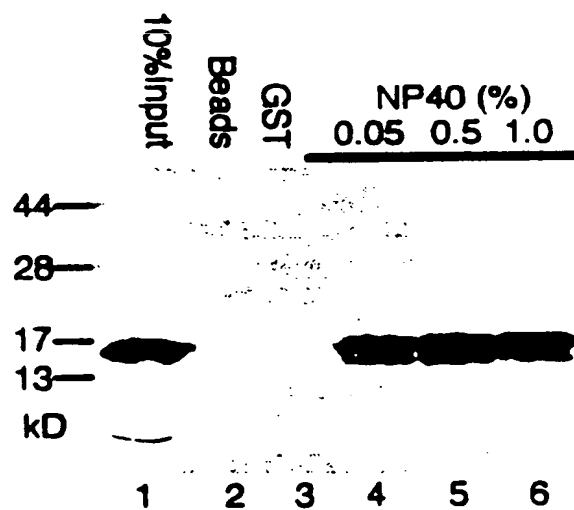
55250" 2E420460

FIGURE 5A



09407432.092999

FIGURE 5B



09407432 092299

### HCV Core Protein-DBX Interaction

[illegible]

FIGURE 6B

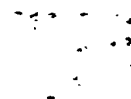
**DBX**



**PL10**



**Ded1p**



09407420760



FIGURE 7A

CORE

DBX

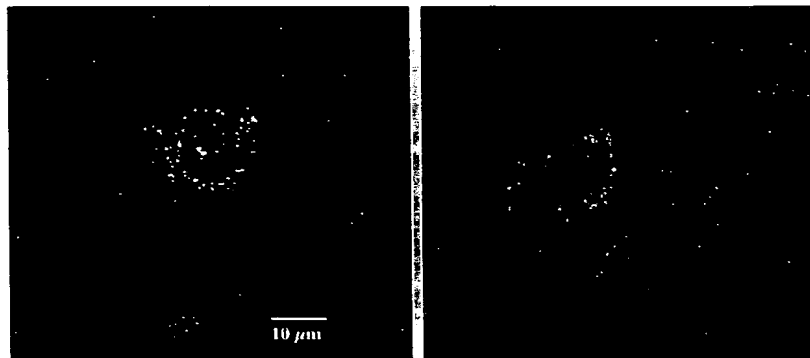
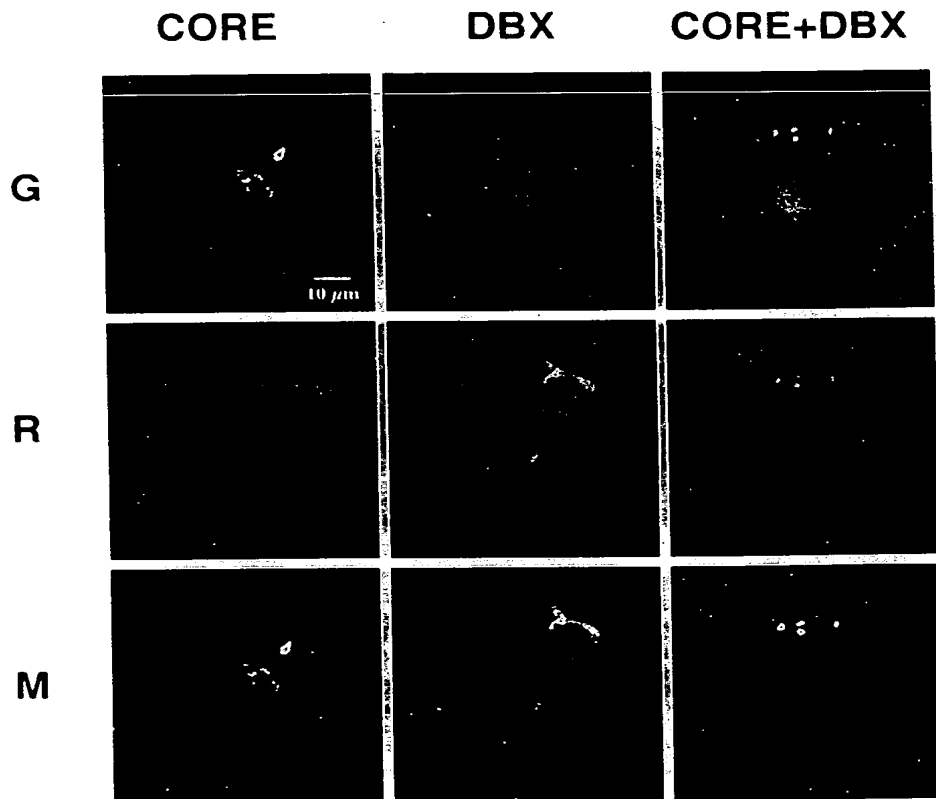
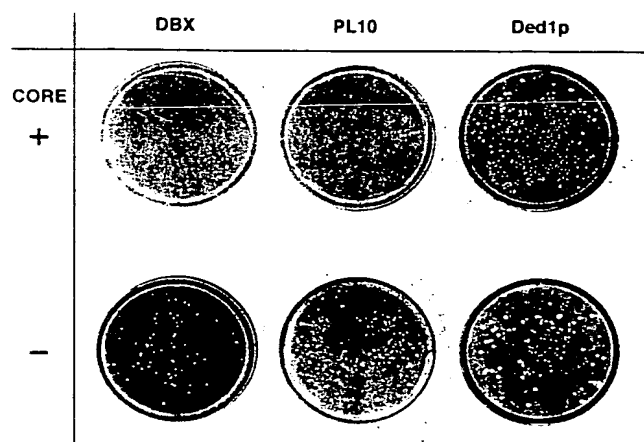


FIGURE 7B



666250 2240460

FIGURE 8



00407432 092990

Figure 9

